| EXPRESS MAIL CERTIFICATE | | | |
|---|---|---|---|
| I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. § 1.10 on the date indicated below and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231. | | | |
| **Typed or Printed Name** | Cloyd Bigalbal | **Express Mail No.** | EL 563 387 369 US |
| **Signature** | | **Date** 04/17/01 | |

| | | |
|---|---|---|
| **SUBMISSION OF SEQUENCE LISTING UNDER 37 CFR §§1.821-1.825** | Attorney Docket | STAN110CON |
| | First Named Inventor | Butcher et al. |
| | Application Number | Unassigned |
| | Filing Date | Herewith (April 17, 2001) |
| Address to:<br>Assistant Commissioner for Patents<br>Box Patent Application<br>Washington, D.C. 20231 | Group Art Unit | Unassigned |
| | Examiner Name | Unassigned |
| | Title: "MODULATION OF SYSTEMIC MEMORY T CELL TRAFFICKING" | |

Sir:

A Sequence Listing in computer readable form as required by 37 CFR §1.821(e) and in compliance with the requirements of 37 CFR §1.824 is submitted herewith. In addition, applicant submits a paper copy of the Sequence Listing as required under 37 CFR §1.821(c) and a statement under 37 CFR §1.821(f).

I hereby state that this Sequence Listing submission, filed in accordance with 37 CFR §1.821(g), does not contain new matter. Furthermore, pursuant to 37 CFR §1.821(f), I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same and that the sequence listings contain no new matter.

The Sequence Listing was prepared with the software FASTSEQ, and conforms with the Patent Office guidelines. Applicant respectfully submits that the subject application is in adherence to 37 CFR §§1.821-1.825.

Respectfully submitted,

Dated: April 17, 2001

By: _____
Pamela J. Sherwood
Registration No. 36,677

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F:\DOCUMENT\STAN (Stanford)\110con\Sequence Certification

SEQUENCE LISTING

<110> Butcher, Eugene C.
Campbell, James J.
Rottman, James B.
Wu, Lijan

<120> Modulation of Systemic Memory T Cell Trafficking

<130> STAN-110CON

<140> Unassigned
<141> 2001-04-17

<150> 09/232,878
<151> 1999-01-15

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<170> FastSEQ for Windows Version 4.0

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<223> CCR4, Chemokine receptor coding sequence

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agaaaagcaa gctgcttctg gttgggccca gacctgcctt gaggagcctg tagagttaaa    180
aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata       227
   Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile
    1               5                  10                  15

tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa      275
Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
                20                  25                  30

gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc      323
Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser
            35                  40                  45

ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc      371
Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
        50                  55                  60

ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc      419
Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
    65                  70                  75

aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg      467
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Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp
 80                  85                  90                  95

ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag      515
Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys
                100                 105                 110

atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt      563
Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe
            115                 120                 125

gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg      611
Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val
        130                 135                 140

ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg      659
Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu
    145                 150                 155

gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc      707
Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe
160                 165                 170                 175

agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac      755
Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr
                180                 185                 190

tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac      803
Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn
            195                 200                 205

att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc      851
Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser
        210                 215                 220

atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag      899
Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys
    225                 230                 235

gcg gtg aag atg atc ttt gcc gtg gtg gtc ctc ttc ctt ggg ttc tgg      947
Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp
240                 245                 250                 255

aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa      995
Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu
                260                 265                 270

gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag     1043
Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln
            275                 280                 285

gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc     1091
Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile
        290                 295                 300

tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc     1139
Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe
    305                 310                 315
```

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aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc     1187
Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu
320                 325                 330                 335

caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc     1235
Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr
                340                 345                 350

atg gat cat gat ctt cat gat gct ctg tag gaaaaatgaa atggtgaaat       1285
Met Asp His Asp Leu His Asp Ala Leu  *
            355                 360

gcagagtcaa tgaacttttc cacattcaga gcttacttta aaattggtat ttttaggtaa   1345
gagatccctg agccagtgtc aggaggaagg cttacaccca cagtggaaag acagcttctc   1405
atcctgcagg cagctttttc tctcccacta gacaagtcca gcctggcaag ggttcacctg   1465
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taacctgaac tgatgggttt ctccagaggg aattgcagag tactggctga tggagtaaat   1645
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<213> H. sapiens

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Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
            20                  25                  30
Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
        35                  40                  45
Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
    50                  55                  60
Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65                  70                  75                  80
Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
                85                  90                  95
Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
            100                 105                 110
Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
        115                 120                 125
Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
    130                 135                 140
Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145                 150                 155                 160
Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
                165                 170                 175
Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
            180                 185                 190
Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
        195                 200                 205
Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
    210                 215                 220
Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
225                 230                 235                 240
Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
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```
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Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
            260                 265                 270
Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
        275                 280                 285
Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
    290                 295                 300
Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
305                 310                 315                 320
Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
                325                 330                 335
Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
            340                 345                 350
Asp His Asp Leu His Asp Ala Leu
        355                 360
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<221> CDS
<222> (53)...(337)
<223> Coding sequence for TARC chemokine

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                                                          Met Ala
                                                           1

cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg      106
Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu
         5                  10                  15

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc      154
Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
     20                  25                  30

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg      202
Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
 35                  40                  45                  50

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act      250
Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
                 55                  60                  65

gtg cag ggc agg gcc atc tgt tcg gac ccc aac aac aag aga gtg aag      298
Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
             70                  75                  80

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tga agcctcctca       347
Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser  *
         85                  90

ccccagactc ctgactgtct cccgggacta cctgggacct ccaccgttgg tgttcaccgc    407
ccccaccctg agcgcctggg tccaggggag gccttccagg gacgaagaag agccacagtg    467
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tctttatcct c 538

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Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu
            20                  25                  30
Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
        35                  40                  45
Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
    50                  55                  60
Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
65                  70                  75                  80
Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
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<213> H. sapiens

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<223> Coding sequence for MDC chemokine

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ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac      100
Leu Val Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
            15                  20                  25

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac      148
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
        30                  35                  40

cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc      196
Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
    45                  50                  55

tgc ccg agg cct ggc gtg gtg ttg cta acc ttc agg gat aag gag atc      244
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile
60                  65                  70                  75

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg      292
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
                80                  85                  90

agc caa tga agagcctact ctgatgaccg tggccttggc tcctccagga             341
Ser Gln  *
```

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<212> PRT
<213> H. sapiens

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            20                  25                  30
Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
        35                  40                  45

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Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
    50                  55                  60
Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
65                  70                  75                  80
Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
                85                  90
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